



-1-

SEQUENCE LISTING

<110> Gardella, Thomas J.
Kronenberg, Henry M.
Potts, John T.
Juppner, Harald

<120> PTH Functional Domain Conjugate Peptides, Derivatives
Thereof and Novel Tethered Ligand-Receptor Molecules

<130> 0609.4780001

<140> US 09/475,158

<141> 1999-12-30

<150> US 60/114,577

<151> 1998-12-31

<160> 67

<170> PatentIn Ver. 2.1

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<212> PRT

<213> Homo sapiens

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Ala Val Ser Glu Ile Gln Leu Met His
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<210> 2

<211> 17

<212> PRT

<213> Homo sapiens

<400> 2

Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp
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Val

<210> 3

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
sequence

<400> 3

Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Leu Asn
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

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<400> 4
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1 5

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<213> Artificial Sequence

<220>
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sequence

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1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

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1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 7
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<213> Homo sapiens

<400> 7
Ala Val Ser Glu His Gln Leu Leu His
1 5

<210> 8
<211> 17
<212> PRT
<213> Homo sapiens

<400> 8
Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu
1 5 10 15

Ile

<210> 9
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<220>
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 1 5 10 15
 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 20 25 30

<210> 10
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 <213> Homo sapiens

<400> 10
 Ala Val Ser Glu His
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<210> 11
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<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 11
 Ala Val Ser Glu Ile Gln Leu Met His Gly Gly Gly Gly Gly Gly Gly
 1 5 10 15
 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 20 25 30

<210> 12
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 12
 Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
 1 5 10 15

<210> 13
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 13
Ala Val Ser Glu Ile Gly Gly Gly Gly Gly Gly Gly Gly Gly Leu Asn
1 5 10 15
Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
20 25 30

<210> 14
<211> 93
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 14
gcuguuuccg aaauccagcu gaugcacggu ggugguggug gucugaacuc cauggaacgu 60
guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 15
<211> 93
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
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guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 16
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

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guugaauggc ugcguaaaaa acugcaggac guu 93

<210> 17
<211> 34
<212> PRT
<213> Homo sapiens

<400> 17
Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn
1 5 10 15

Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His
 20 25 30

Asn Phe

<210> 18
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 18
 Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly Lys Ser Ile Gln
 1 5 10 15
 Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile His
 20 25 30

Thr Ala

<210> 19
 <211> 37
 <212> PRT
 <213> Homo sapiens

<400> 19
 His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln
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 Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu Gly Lys Arg Tyr Lys
 20 25 30

Gln Arg Val Asn Lys
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 <212> PRT
 <213> Homo sapiens

<400> 20
 His Ser Asp Ala Val Phe Thr Asp Asn Tyr Thr Arg Leu Arg Lys Gln
 1 5 10 15
 Met Ala Val Lys Lys Tyr Leu Asn Ser Ile Leu Asn
 20 25

<210> 21
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 <212> PRT
 <213> Homo sapiens

<400> 21
 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
 1 5 10 15
 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg

20

25

<210> 22
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<212> PRT
<213> Homo sapiens

<400> 22
His Ala Asp Gly Val Phe Thr Ser Asp Phe Ser Lys Leu Leu Gly Gln
1 5 10 15
Leu Ser Ala Lys Lys Tyr Leu Glu Ser Leu Met
20 25

<210> 23
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<212> PRT
<213> Homo sapiens

<400> 23
His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15
Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
20 25 30

<210> 24
<211> 29
<212> PRT
<213> Homo sapiens

<400> 24
His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Ser
1 5 10 15
Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
20 25

<210> 25
<211> 42
<212> PRT
<213> Homo sapiens

<400> 25
Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys
1 5 10 15
Ile His Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys Gly Lys
20 25 30
Lys Asn Asp Trp Lys His Asn Ile Thr Gln
35 40

<210> 26
<211> 27
<212> PRT

<213> Homo sapiens

<400> 26

His Ser Asp Gly Thr Phe Thr Ser Glu Leu Ser Arg Leu Arg Glu Gly
1 5 10 15

Ala Arg Leu Gln Arg Leu Leu Gln Gly Leu Val
20 25

<210> 27

<211> 32

<212> PRT

<213> Homo sapiens

<400> 27

Cys Gly Asn Leu Ser Thr Cys Met Leu Gly Thr Tyr Thr Gln Asp Phe
1 5 10 15

Asn Lys Phe His Thr Phe Pro Gln Thr Ala Ile Gly Val Gly Ala Pro
20 25 30

<210> 28

<211> 37

<212> PRT

<213> Homo sapiens

<400> 28

Ala Cys Asn Thr Ala Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu
1 5 10 15

Ser Arg Ser Gly Gly Met Val Lys Ser Asn Phe Val Pro Thr Asn Val
20 25 30

Gly Ser Lys Ala Phe
35

<210> 29

<211> 37

<212> PRT

<213> Homo sapiens

<400> 29

Ala Cys Asp Thr Ala Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu
1 5 10 15

Ser Arg Ser Gly Gly Val Val Lys Asn Asn Phe Val Pro Thr Asn Val
20 25 30

Gly Ser Lys Ala Phe
35

<210> 30

<211> 37

<212> PRT

<213> Homo sapiens

<400> 30
Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
1 5 10 15
Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val
20 25 30
Gly Ser Asn Thr Tyr
35

<210> 31
<211> 36
<212> PRT
<213> Homo sapiens

<400> 31
Gly Cys Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile
1 5 10 15
Tyr Gln Phe Thr Asp Lys Asp Lys Asp Asn Val Ala Pro Arg Ser Lys
20 25 30
Ile Ser Pro Gln
35

<210> 32
<211> 41
<212> PRT
<213> Homo sapiens

<400> 32
Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg
1 5 10 15
Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His
20 25 30
Ser Asn Arg Lys Leu Met Glu Ile Ile
35 40

<210> 33
<211> 40
<212> PRT
<213> Homo sapiens

<400> 33
Glu Glu Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys
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Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn
20 25 30
Asn Arg Leu Leu Leu Asp Thr Ile
35 40

<210> 34
<211> 46
<212> PRT

<213> Homo sapiens

<400> 34

Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg
 1 5 10 15
 Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln
 20 25 30
 Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile
 35 40 45

<210> 35

<211> 63

<212> PRT

<213> Homo sapiens

<400> 35

Cys Asp Ala Thr Cys Gln Phe Arg Lys Ala Ile Asp Asp Cys Gln Lys
 1 5 10 15
 Gln Ala His His Ser Asn Val Leu Gln Thr Ser Val Gln Thr Thr Ala
 20 25 30
 Thr Phe Thr Ser Met Asp Thr Ser Gln Leu Pro Gly Asn Ser Val Phe
 35 40 45
 Lys Glu Cys Met Lys Gln Lys Lys Lys Glu Phe Ser Ser Gly Lys
 50 55 60

<210> 36

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>

<221> CDS

<222> (1)..(1332)

<400> 36

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 1 5 10 15
 cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga 96
 Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
 20 25 30
 gga ggc gag gta ttt gac cgc cta ggc atg atc tac acc gtg gga tac 144
 Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 35 40 45
 tcc atg tct ctc gcc tcc ctc acg gtg gct gtg ctc atc ctg gcc tat 192
 Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
 50 55 60

ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac atg ttc	240
Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe	
65 70 75 80	
ctg tgc ttt atg ctg cgc gcc gcg agc atc ttc gtg aag gac gct gtg	288
Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val	
85 90 95	
ctc tac tct ggc ttc acg ctg gat gag gcc gag cgc ctc aca gag gaa	336
Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu	
100 105 110	
gag ttg cac atc atc gcg cag gtg cca cct ccg ccg gcc gct gcc gcc	384
Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala	
115 120 125	
gta ggc tac gct ggc tgc cgc gtg gcg gtg acc ttc ttc ctc tac ttc	432
Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe	
130 135 140	
ctg gct acc aac tac tac tgg atc ctg gtg gag ggg ctg tac ttg cac	480
Leu Ala Thr Asn Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His	
145 150 155 160	
agc ctc atc ttc atg gcc ttt ttc tca gag aag aag tac ctg tgg ggc	528
Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly	
165 170 175	
ttc acc atc ttt ggc tgg ggt cta ccg gct gtc ttc gtg gct gtg tgg	576
Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp	
180 185 190	
gtc ggt gtc aga gca acc ttg gcc aac act ggg tgc tgg gat ctg agc	624
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser	
195 200 205	
tcc ggg cac aag aag tgg atc atc cag gtg ccc atc ctg gca tct gtt	672
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val	
210 215 220	
gtg ctc aac ttc atc ctt ttt atc aac atc atc cgg gtg ctt gcc act	720
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr	
225 230 235 240	
aag ctt cgg gag acc aat gcg ggc cgg tgt gac acc agg cag cag tac	768
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr	
245 250 255	
cgg aag ctg ctc agg tcc acg ttg gtg ctc gtg ccg ctc ttt ggt gtg	816
Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val	
260 265 270	
cac tac acc gtc ttc atg gcc ttg ccg tac acc gag gtc tca ggg aca	864
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr	
275 280 285	
ttg tgg cag atc cag atg cat tat gag atg ctc ttc aac tcc ttc cag	912
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln	
290 295 300	
gga ttt ttt gtt gcc atc ata tac tgt ttc tgc aat ggt gag gtg cag	960
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln	

305	310	315	320	
gca gag att agg aag tca tgg agc cgc tgg aca ctg gcg ttg gac ttc				1008
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe				
	325	330	335	
aag cgc aaa gca cga agt ggg agt agc agc tac agc tat ggc cca atg				1056
Lys Arg Lys Ala Arg Ser Gly Ser Ser Tyr Ser Tyr Gly Pro Met				
	340	345	350	
gtg tct cac acg agt gtg acc aat gtg ggc ccc cgt gca gga ctc agc				1104
Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser				
	355	360	365	
ctc ccc ctc agc ccc cgc ctg cct cct gcc act acc aat ggc cac tcc				1152
Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser				
	370	375	380	
cag ctg cct ggc cat gcc aag cca ggg gct cca gcc act gag act gaa				1200
Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu				
	385	390	395	400
acc cta cca gtc act atg gcg gtt ccc aag gac gat gga ttc ctt aac				1248
Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn				
	405	410	415	
ggc tcc tgc tca ggc ctg gat gag gag gcc tcc ggg tct gcg cgg ccg				1296
Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro				
	420	425	430	
cct cca ttg ttg cag gaa gga tgg gaa aca gtc atg tga				1335
Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met				
	435	440		

<210> 37
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 37
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
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 Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
 20 25 30
 Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 35 40 45
 Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
 50 55 60
 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe
 65 70 75 80
 Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val
 85 90 95
 Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu
 100 105 110
 Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Ala Ala Ala Ala
 115 120 125

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Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe
130 135 140
Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His
145 150 155 160
Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly
165 170 175
Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp
180 185 190
Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser
195 200 205
Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Val
210 215 220
Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr
225 230 235 240
Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr
245 250 255
Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val
260 265 270
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr
275 280 285
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln
290 295 300
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln
305 310 315 320
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe
325 330 335
Lys Arg Lys Ala Arg Ser Gly Ser Ser Tyr Ser Tyr Gly Pro Met
340 345 350
Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala Gly Leu Ser
355 360 365
Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn Gly His Ser
370 375 380
Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr Glu Thr Glu
385 390 395 400
Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly Phe Leu Asn
405 410 415
Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser Ala Arg Pro
420 425 430
Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met
435 440

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<210> 38
 <211> 1002
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1002)

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<400> 38
atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc 48
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1 5 10 15
cca gtg ctc agc tcc gcc tat gcg gcc gaa acc agc gag cac ggc gga 96

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Pro	Val	Leu	Ser	Ser	Ala	Tyr	Ala	Ala	Glu	Thr	Ser	Glu	His	Gly	Gly		
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Gly	Gly	Glu	Val	Phe	Asp	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr		
		35					40				45						
tcc	atg	tct	ctc	gcc	tcc	ctc	acg	gtg	gct	gtg	ctc	atc	ctg	gcc	tat	192	
Ser	Met	Ser	Leu	Ala	Ser	Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Ala	Tyr		
		50				55					60						
ttt	agg	cgg	ctg	cac	tgc	acg	cgc	aac	tac	atc	cac	atg	cac	atg	ttc	240	
Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Met	Phe		
	65				70				75						80		
ctg	tgc	ttt	atg	ctg	cgc	gcc	gcg	agc	atc	ttc	gtg	aag	gac	gct	gtg	288	
Leu	Ser	Phe	Met	Leu	Arg	Ala	Ala	Ser	Ile	Phe	Val	Lys	Asp	Ala	Val		
				85					90					95			
ctc	tac	tct	ggc	ttc	acg	ctg	gat	gag	gcc	gag	cgc	ctc	aca	gag	gaa	336	
Leu	Tyr	Ser	Gly	Phe	Thr	Leu	Asp	Glu	Ala	Glu	Arg	Leu	Thr	Glu	Glu		
			100					105					110				
gag	ttg	cac	atc	atc	gcg	cag	gtg	cca	cct	ccg	ccg	gcc	gct	gcc	gcc	384	
Glu	Leu	His	Ile	Ile	Ala	Gln	Val	Pro	Pro	Pro	Pro	Ala	Ala	Ala	Ala		
		115					120					125					
gta	ggc	tac	gct	ggc	tgc	cgc	gtg	gcg	gtg	acc	ttc	ttc	ctc	tac	ttc	432	
Val	Gly	Tyr	Ala	Gly	Cys	Arg	Val	Ala	Val	Thr	Phe	Phe	Leu	Tyr	Phe		
		130				135					140						
ctg	gct	acc	aac	tac	tac	tgg	atc	ctg	gtg	gag	ggg	ctg	tac	ttg	cac	480	
Leu	Ala	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His		
	145				150					155					160		
agc	ctc	atc	ttc	atg	gcc	ttt	ttc	tca	gag	aag	aag	tac	ctg	tgg	ggc	528	
Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	Glu	Lys	Lys	Tyr	Leu	Trp	Gly		
				165					170					175			
ttc	acc	atc	ttt	ggc	tgg	ggt	cta	ccg	gct	gtc	ttc	gtg	gct	gtg	tgg	576	
Phe	Thr	Ile	Phe	Gly	Trp	Gly	Leu	Pro	Ala	Val	Phe	Val	Ala	Val	Trp		
			180					185					190				
gtc	ggt	gtc	aga	gca	acc	ttg	gcc	aac	act	ggg	tgc	tgg	gat	ctg	agc	624	
Val	Gly	Val	Arg	Ala	Thr	Leu	Ala	Asn	Thr	Gly	Cys	Trp	Asp	Leu	Ser		
		195					200					205					
tcc	ggg	cac	aag	aag	tgg	atc	atc	cag	gtg	ccc	atc	ctg	gca	tct	gtt	672	
Ser	Gly	His	Lys	Lys	Trp	Ile	Ile	Gln	Val	Pro	Ile	Leu	Ala	Ser	Val		
		210				215					220						
gtg	ctc	aac	ttc	atc	ctt	ttt	atc	aac	atc	atc	cgg	gtg	ctt	gcc	act	720	
Val	Leu	Asn	Phe	Ile	Leu	Phe	Ile	Asn	Ile	Ile	Arg	Val	Leu	Ala	Thr		
	225				230					235					240		
aag	ctt	cgg	gag	acc	aat	gcg	ggc	cgg	tgt	gac	acc	agg	cag	cag	tac	768	
Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr	Arg	Gln	Gln	Tyr		
				245					250					255			
cgg	aag	ctg	ctc	agg	tcc	acg	ttg	gtg	ctc	gtg	ccg	ctc	ttt	ggt	gtg	816	
Arg	Lys	Leu	Leu	Arg	Ser	Thr	Leu	Val	Leu	Val	Pro	Leu	Phe	Gly	Val		
				260				265						270			

cac tac acc gtc ttc atg gcc ttg ccg tac acc gag gtc tca ggg aca	864
His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val Ser Gly Thr	
275 280 285	
ttg tgg cag atc cag atg cat tat gag atg ctc ttc aac tcc ttc cag	912
Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln	
290 295 300	
gga ttt ttt gtt gcc atc ata tac tgt ttc tgc aat ggt gag gtg cag	960
Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln	
305 310 315 320	
gca gag att agg aag tca tgg agc cgc tgg aca ctg gcg tag	1002
Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala	
325 330	

<210> 39
 <211> 333
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 39
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Ala Glu Thr Ser Glu His Gly Gly
 20 25 30
 Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 35 40 45
 Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu Ala Tyr
 50 55 60
 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Met Phe
 65 70 75 80
 Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys Asp Ala Val
 85 90 95
 Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu
 100 105 110
 Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Pro Ala Ala Ala Ala
 115 120 125
 Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe
 130 135 140
 Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His
 145 150 155 160
 Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly
 165 170 175
 Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp
 180 185 190
 Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser
 195 200 205
 Ser Gly His Lys Lys Trp Ile Gln Val Pro Ile Leu Ala Ser Val
 210 215 220
 Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr
 225 230 235 240
 Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr
 245 250 255
 Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu Phe Gly Val
 260 265 270

His	Tyr	Thr	Val	Phe	Met	Ala	Leu	Pro	Tyr	Thr	Glu	Val	Ser	Gly	Thr
		275					280					285			
Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	Met	Leu	Phe	Asn	Ser	Phe	Gln
	290					295					300				
Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	Phe	Cys	Asn	Gly	Glu	Val	Gln
305					310					315					320
Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	Trp	Thr	Leu	Ala			
				325					330						

<210> 40
 <211> 975
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(972)

<400> 40	
atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta ctc tgc tgc	48
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys	
1 5 10 15	
cca gtg ctc agc tcc gca tat gcg ctg gag gta ttt gac cgc cta ggc	96
Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly	
20 25 30	
atg atc tac acc gtg gga tac tcc atg tct ctc gcc tcc ctc acg gtg	144
Met Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val	
35 40 45	
gct gtg ctc atc ctg gcc tat ttt agg cgg ctg cac tgc acg cgc aac	192
Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn	
50 55 60	
tac atc cac atg cac atg ttc ctg tcg ttt atg ctg cgc gcc gcg agc	240
Tyr Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser	
65 70 75 80	
atc ttc gtg aag gac gct gtg ctc tac tct ggc ttc acg ctg gat gag	288
Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu	
85 90 95	
gcc gag cgc ctc aca gag gaa gag ttg cac atc atc gcg cag gtg cca	336
Ala Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro	
100 105 110	
cct ccg ccg gcc gct gcc gcc gta ggc tac gct ggc tgc cgc gtg gcg	384
Pro Pro Pro Ala Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala	
115 120 125	
gtg acc ttc ttc ctc tac ttc ctg gct acc aac tac tac tgg atc ctg	432
Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu	
130 135 140	

gtg gag ggg ctg tac ttg cac agc ctc atc ttc atg gcc ttt ttc tca	480
Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser	
145 150 155 160	
gag aag aag tac ctg tgg ggc ttc acc atc ttt ggc tgg ggt cta ccg	528
Glu Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro	
165 170 175	
gct gtc ttc gtg gct gtg tgg gtc ggt gtc aga gca acc ttg gcc aac	576
Ala Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn	
180 185 190	
act ggg tgc tgg gat ctg agc tcc ggg cac aag aag tgg atc atc cag	624
Thr Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln	
195 200 205	
gtg ccc atc ctg gca tct gtt gtg ctc aac ttc atc ctt ttt atc aac	672
Val Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn	
210 215 220	
atc atc cgg gtg ctt gcc act aag ctt cgg gag acc aat gcg ggc cgg	720
Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg	
225 230 235 240	
tgt gac acc agg cag cag tac cgg aag ctg ctc agg tcc acg ttg gtg	768
Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val	
245 250 255	
ctc gtg ccg ctc ttt ggt gtg cac tac acc gtc ttc atg gcc ttg ccg	816
Leu Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro	
260 265 270	
tac acc gag gtc tca ggg aca ttg tgg cag atc cag atg cat tat gag	864
Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu	
275 280 285	
atg ctc ttc aac tcc ttc cag gga ttt ttt gtt gcc atc ata tac tgt	912
Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys	
290 295 300	
ttc tgc aat ggt gag gtg cag gca gag att agg aag tca tgg agc cgc	960
Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg	
305 310 315 320	
tgg aca ctg gcg tag	975
Trp Thr Leu Ala	

<210> 41
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 41
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Leu Glu Val Phe Asp Arg Leu Gly

[illegible]

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<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence
```

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<220>  
<221> UNSURE  
<222> (1)..(1)  
<223> May be any amino acid.
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<220>  
<221> UNSURE  
<222> (3)..(3)  
<223> May be any amino acid.
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<220>  
<221> UNSURE  
<222> (5)..(8)  
<223> May be any amino acid.
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$\langle 220 \rangle$

<223> Description of Artificial Sequence: synthetic polypeptide

<400> 42

Xaa Val Xaa Glu Xaa Xaa Xaa Xaa His
1 5

<210> 43

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (1)..(5)

<223> May be any amino acid.

<220>

<221> UNSURE

<222> (7)..(8)

<223> May be any amino acid.

<220>

<221> UNSURE

<222> (10)

<223> May be any amino acid.

<220>

<221> UNSURE

<222> (12)

<223> May be any amino acid.

<220>

<221> UNSURE

<222> (15)..(16)

<223> May be any amino acid.

<220>

<223> Description of Artificial Sequence: synthetic Polypeptide

<400> 43

Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Trp Xaa Leu Xaa Lys Leu Xaa Xaa
1 5 10 15

Val

<210> 44

<211> 9

<212> PRT

<213> Homo sapiens

<400> 44

Ser Val Ser Glu Ile Gln Leu Met His
1 5

<210> 45

<211> 17
<212> PRT
<213> Homo sapiens

<400> 45
Leu Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln
1 5 10 15

Asp Val

<210> 46
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 46
atggggggccg cccggatcgc acccagcctg gcgctcctac tctgctgccc agtgctcagc 60
tccgcatatg cgctggtgga tgcggacgat gtctttacca aagaggaaca gattttcctg 120

<210> 47
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 47
aaccggacgt gggccaacta cagcgagtgc ctcaagttca tgaccaatga gaccgaggaa 60
cgggaggtat ttgaccgcct aggcgatgac tacaccgtgg gatactccat gtctctcgcc 120

<210> 48
<211> 39
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 48
gcguuuuccg aaauccagcu gaugcacggc ggaggaggc

39

<210> 49
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 49

ctctgctgcc cagtgtcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtatttga ccgcctaggc atgatctac 99

<210> 50
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 50
ctctgctgcc cagtgtcag ctccgcctat gcggtttccg aaatccagct gatgcacggc 60
ggaggaggcg aggtatttga ccgcctaggc atgatctac 99

<210> 51
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
oligonucleotide

<400> 51
ctctgctgcc cagtgtcag ctccgcatat ccctacgacg tccccgacta cgccggcgga 60
ggaggcgagg tatttgaccg cctaggcatg atctac 96

<210> 52
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 52
ctctgctgcc cagtgtcag ctccgcatat ccctacgacg tccccgacta cgccggcgga 60
ggaggcgagg tatttgaccg cctaggcatg atctac 96

<210> 53
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 53
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Cys Cys
1 5 10 15
Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Phe
20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu
35 40

<210> 54
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 54
Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn
1 5 10 15
Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
20 25 30
Val Gly Tyr Ser Met Ser Leu Ala
35 40

<210> 55
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 55
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln
1 5 10 15
Leu Met His Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile
20 25 30
Tyr

<210> 56
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 56
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Pro Tyr Asp Val Pro Asp
1 5 10 15
Tyr Ala Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
20 25 30

<210> 57
 <211> 1380
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1353)

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<400> 57
atg ggg acc gcc cgg atc gca ccc ggc ctg gcg ctc ctg ctc tgc tgc      48
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
  1                               5                               10                               15

ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cat      96
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
                20                25                30

aat cgt ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac      144
Asn Arg Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
                35                40                45

acc gtg ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc      192
Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu
  50                55                60

atc ctg gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac      240
Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His
  65                70                75                80

atg cac ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc      288
Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val
                85                90                95

aag gac gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc      336
Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg
                100                105                110

ctc acc gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct      384
Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro
                115                120                125

gcc acc gcc gct gcc ggc tac gcg ggc tgc agg gtg gct gtg acc ttc      432
Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe
                130                135                140

ttc ctt tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg      480
Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly
                145                150                155                160

ctg tac ctg cac agc ctc atc ttc atg gcc ttc ttc tca gag aag aag      528
Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys
                165                170                175

tac ctg tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc      576
Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe
                180                185                190

```

gtg gct gtg tgg gtc agt gtc aga gct acc ctg gcc aac acc ggg tgc Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys 195 200 205	624
tgg gac ttg agc tcc ggg aac aaa aag tgg atc atc cag gtg ccc atc Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile 210 215 220	672
ctg gcc tcc att gtg ctc aac ttc atc ctc ttc atc aat atc gtc cgg Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg 225 230 235 240	720
gtg ctc gcc acc aag ctg cgg gag acc aac gcc ggc cgg tgt gac aca Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr 245 250 255	768
cgg cag cag tac cgg aag ctg ctc aaa tcc acg ctg gtg ctc atg ccc Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro 260 265 270	816
ctc ttt ggc gtc cac tac att gtc ttc atg gcc aca cca tac acc gag Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu 275 280 285	864
gtc tca ggg acg ctc tgg caa gtc cag atg cac tat gag atg ctc ttc Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe 290 295 300	912
aac tcc ttc cag gga ttt ttt gtc gca atc ata tac tgt ttc tgc aat Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn 305 310 315 320	960
ggc gag gta caa gct gag atc aag aaa tct tgg agc cgc tgg aca ctg Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu 325 330 335	1008
gca ctg gac ttc aag cga aag gca cgc agc ggg agc agc agc tat agc Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser 340 345 350	1056
tac ggc ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg 355 360 365	1104
gtg gga ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr 370 375 380	1152
acc aac ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro 385 390 395 400	1200
gcc ctg gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys 405 410 415	1248
gac gat ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala 420 425 430	1296
tct ggg cct gag cgg cca cct gcc ctg cta cag gaa gag tgg gag aca Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr 1344	

435 440 445 1380
gtc atg tga ccaggcgctg ggggctggac ctgctga
Val Met
450

<210> 58
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

<400> 58
Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
1 5 10 15
Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
20 25 30
Asn Arg Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr
35 40 45
Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu
50 55 60
Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His
65 70 75 80
Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val
85 90 95
Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg
100 105 110
Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro
115 120 125
Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe
130 135 140
Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly
145 150 155 160
Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys
165 170 175
Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe
180 185 190
Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys
195 200 205
Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile
210 215 220
Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg
225 230 235 240
Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr
245 250 255
Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro
260 265 270
Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu
275 280 285
Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe
290 295 300
Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn
305 310 315 320
Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu
325 330 335
Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser
340 345 350
Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg

[illegible]

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<210> 59
<211> 1380
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: modified PTH
receptor sequence

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<220>  
<221> CDS  
<222> (28) .. (1335)
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ggc tgc agg gtg gct gtg acc ttc ttc ctt tac ttc ctg gcc acc aac Gly Cys Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn 125 130 135	438
tac tac tgg att ctg gtg gag ggg ctg tac ctg cac agc ctc atc ttc Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe 140 145 150	486
atg gcc ttc ttc tca gag aag aag tac ctg tgg ggc ttc aca gtc ttc Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe 155 160 165	534
ggc tgg ggt ctg ccc gct gtc ttc gtg gct gtg tgg gtc agt gtc aga Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg 170 175 180 185	582
gct acc ctg gcc aac acc ggg tgc tgg gac ttg agc tcc ggg aac aaa Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys 190 195 200	630
aag tgg atc atc cag gtg ccc atc ctg gcc tcc att gtg ctc aac ttc Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe 205 210 215	678
atc ctc ttc atc aat atc gtc cgg gtg ctc gcc acc aag ctg cgg gag Ile Leu Phe Ile Asn Ile Val Arg Val Leu Ala Thr Lys Leu Arg Glu 220 225 230	726
acc aac gcc ggc cgg tgt gac aca cgg cag cag tac cgg aag ctg ctc Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu 235 240 245	774
aaa tcc acg ctg gtg ctc atg ccc ctc ttt ggc gtc cac tac att gtc Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val 250 255 260 265	822
ttc atg gcc aca cca tac acc gag gtc tca ggg acg ctc tgg caa gtc Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Val 270 275 280	870
cag atg cac tat gag atg ctc ttc aac tcc ttc cag gga ttt ttt gtc Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val 285 290 295	918
gca atc ata tac tgt ttc tgc aat ggc gag gta caa gct gag atc aag Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys 300 305 310	966
aaa tct tgg agc cgc tgg aca ctg gca ctg gac ttc aag cga aag gca Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala 315 320 325	1014
cgc agc ggg agc agc agc tat agc tac ggc ccc atg gtg tcc cac aca Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr 330 335 340 345	1062
agt gtg acc aat gtc ggc ccc cgt gtg gga ctc ggc ctg ccc ctc agc Ser Val Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser 350 355 360	1110
ccc cgc cta ctg ccc act gcc acc acc aac ggc cac cct cag ctg cct Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn Gly His Pro Gln Leu Pro	1158

365	370	375	
ggc cat gcc aag cca ggg acc cca gcc ctg gag acc ctc gag acc aca			1206
Gly His Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr			
380	385	390	
cca cct gcc atg gct gct ccc aag gac gat ggg ttc ctc aac ggc tcc			1254
Pro Pro Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Asn Gly Ser			
395	400	405	
tgc tca ggc ctg gac gag gag gcc tct ggg cct gag cgg cca cct gcc			1302
Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Pro Glu Arg Pro Pro Ala			
410	415	420	425
ctg cta cag gaa gag tgg gag aca gtc atg tga ccaggcgctg ggggctggac			1355
Leu Leu Gln Glu Glu Trp Glu Thr Val Met			
430	435		
ctgctgacat agtggatgga cagat			1380

<210> 60
 <211> 435
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 60
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Glu Val Phe Asp Arg Leu Gly Met Ile
 20 25 30
 Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val
 35 40 45
 Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile
 50 55 60
 His Met His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe
 65 70 75 80
 Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu
 85 90 95
 Arg Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro
 100 105 110
 Pro Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr
 115 120 125
 Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu
 130 135 140
 Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys
 145 150 155 160
 Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val
 165 170 175
 Phe Val Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly
 180 185 190
 Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro
 195 200 205
 Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val
 210 215 220
 Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp
 225 230 235 240

Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met
 245 250 255
 Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr
 260 265 270
 Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu
 275 280 285
 Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys
 290 295 300
 Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr
 305 310 315 320
 Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr
 325 330 335
 Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro
 340 345 350
 Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala
 355 360 365
 Thr Thr Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr
 370 375 380
 Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro
 385 390 395 400
 Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu
 405 410 415
 Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu
 420 425 430
 Thr Val Met
 435

<210> 61
 <211> 1363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<220>
 <221> CDS
 <222> (1)..(1347)

<400> 61
 atg ggg acc gcc cgg atc gca ccc ggc ctg gcg ctc ctg ctc tgc tgc 48
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 ccc gtg ctc agc tcc gcg tac gcg gtt tcc gaa atc cag ctg atg cac 96
 Pro Val Leu Ser Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
 20 25 30
 ggc gga gga ggc gag gtg ttt gac cgc ctg ggc atg att tac acc gtg 144
 Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val
 35 40 45
 ggc tac tcc gtg tcc ctg gcg tcc ctc acc gta gct gtg ctc atc ctg 192
 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu
 50 55 60
 gcc tac ttt agg cgg ctg cac tgc acg cgc aac tac atc cac atg cac 240
 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His
 65 70 75 80

ctg ttc ctg tcc ttc atg ctg cgc gcc gtg agc atc ttc gtc aag gac	288
Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp	
85 90 95	
gct gtg ctc tac tct ggc gcc acg ctt gat gag gct gag cgc ctc acc	336
Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr	
100 105 110	
gag gag gag ctg cgc gcc atc gcc cag gcg ccc ccg ccg cct gcc acc	384
Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala Thr	
115 120 125	
gcc gct gcc ggc tac gcg ggc tgc agg gtg gct gtg acc ttc ttc ctt	432
Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu	
130 135 140	
tac ttc ctg gcc acc aac tac tac tgg att ctg gtg gag ggg ctg tac	480
Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr	
145 150 155 160	
ctg cac agc ctc atc ttc atg gcc ttc ttc tca gag aag aag tac ctg	528
Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu	
165 170 175	
tgg ggc ttc aca gtc ttc ggc tgg ggt ctg ccc gct gtc ttc gtg gct	576
Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala	
180 185 190	
gtg tgg gtc agt gtc aga gct acc ctg gcc aac acc ggg tgc tgg gac	624
Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp	
195 200 205	
ttg agc tcc ggg aac aaa aag tgg atc atc cag gtg ccc atc ctg gcc	672
Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala	
210 215 220	
tcc att gtg ctc aac ttc atc ctc ttc atc aat atc gtc cgg gtg ctc	720
Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu	
225 230 235 240	
gcc acc aag ctg cgg gag acc aac gcc ggc cgg tgt gac aca cgg cag	768
Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln	
245 250 255	
cag tac cgg aag ctg ctc aaa tcc acg ctg gtg ctc atg ccc ctc ttt	816
Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe	
260 265 270	
ggc gtc cac tac att gtc ttc atg gcc aca cca tac acc gag gtc tca	864
Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser	
275 280 285	
ggg acg ctc tgg caa gtc cag atg cac tat gag atg ctc ttc aac tcc	912
Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser	
290 295 300	
ttc cag gga ttt ttt gtc gca atc ata tac tgt ttc tgc aat ggc gag	960
Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu	
305 310 315 320	
gta caa gct gag atc aag aaa tct tgg agc cgc tgg aca ctg gca ctg	1008
Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu	

325	330	335	
gac ttc aag cga aag gca cgc agc ggg agc agc agc tat agc tac ggc			1056
Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly			
340	345	350	
ccc atg gtg tcc cac aca agt gtg acc aat gtc ggc ccc cgt gtg gga			1104
Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly			
355	360	365	
ctc ggc ctg ccc ctc agc ccc cgc cta ctg ccc act gcc acc acc aac			1152
Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn			
370	375	380	
ggc cac cct cag ctg cct ggc cat gcc aag cca ggg acc cca gcc ctg			1200
Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu			
385	390	395	400
gag acc ctc gag acc aca cca cct gcc atg gct gct ccc aag gac gat			1248
Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp			
405	410	415	
ggg ttc ctc aac ggc tcc tgc tca ggc ctg gac gag gag gcc tct ggg			1296
Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly			
420	425	430	
cct gag cgg cca cct gcc ctg cta cag gaa gag tgg gag aca gtc atg			1344
Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met			
435	440	445	
tga ccagggcgtg ggggct			1363

<210> 62
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 receptor sequence

<400> 62
 Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ala Tyr Ala Val Ser Glu Ile Gln Leu Met His
 20 25 30
 Gly Gly Gly Gly Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val
 35 40 45
 Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile Leu
 50 55 60
 Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His
 65 70 75 80
 Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys Asp
 85 90 95
 Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu Thr
 100 105 110
 Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Ala Thr
 115 120 125
 Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe Leu
 130 135 140

Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr
 145 150 155 160
 Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu
 165 170 175
 Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala
 180 185 190
 Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp
 195 200 205
 Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala
 210 215 220
 Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val Leu
 225 230 235 240
 Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln
 245 250 255
 Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe
 260 265 270
 Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser
 275 280 285
 Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser
 290 295 300
 Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu
 305 310 315 320
 Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu
 325 330 335
 Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
 340 345 350
 Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val Gly
 355 360 365
 Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr Asn
 370 375 380
 Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala Leu
 385 390 395 400
 Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp Asp
 405 410 415
 Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly
 420 425 430
 Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val Met
 435 440 445

<210> 63
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 63
 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val
 1 5 10 15

<210> 64
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: modified PTH
 sequence

<400> 64
 Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Gly Ile Gln

1 5 10 15
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
20 25 30

<210> 65
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 65
Ala Val Ser Glu His Gly Gly Gly Gly Gly Gly Gly Gly Ile Gln
1 5 10 15

Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
20 25 30

Sub B1
<210> 66
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

a13
cont
<400> 66
Ala Val Ser Glu His Gln Leu Leu His Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile
20 25 30

<210> 67
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified PTH
sequence

<400> 67
Ala Val Ser Glu Ile Gln Leu Met His Asn Leu
1 5 10